



Patin Dock 1007P1D1seq1 (new)-response to 6-29-04 action.txt  
Patent & Trademark Office

### Sequence Listing

#### (1) GENERAL INFORMATION:

- (i) APPLICANT: Ashkenazi, Avi J.
  - (ii) TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
  - (iii) NUMBER OF SEQUENCES: 28
  - (iv) CORRESPONDENCE ADDRESS:
    - (A) ADDRESSEE: Genentech, Inc.
    - (B) STREET: 1 DNA Way
    - (C) CITY: South San Francisco
    - (D) STATE: California
    - (E) COUNTRY: USA
    - (F) ZIP: 94080
  - (v) COMPUTER READABLE FORM:
    - (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
    - (B) COMPUTER: IBM PC compatible
    - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
    - (D) SOFTWARE: WinPatin (Genentech)
  - (vi) CURRENT APPLICATION DATA:
    - (A) APPLICATION NUMBER: US/09/993,234A
    - (B) FILING DATE: 19-NOV-2001
    - (C) CLASSIFICATION:
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: 08/828683
    - (B) FILING DATE: 31-MAR-1997
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: 08/625328
    - (B) FILING DATE: 1-Apr-1996
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: 08/710802
    - (B) FILING DATE: 23-Sep-1996
  - (viii) ATTORNEY/AGENT INFORMATION:
    - (A) NAME: Marschang, Diane L.
    - (B) REGISTRATION NUMBER: 35,600
    - (C) REFERENCE/DOCKET NUMBER: P1007P1D1
  - (ix) TELECOMMUNICATION INFORMATION:
    - (A) TELEPHONE: 650/225-5416
    - (B) TELEFAX: 650/952-9881
- (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 181 amino acids
  - (B) TYPE: Amino Acid
  - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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Met	Glu	Gln	Arg	Pro	Arg	Gly	Cys	Ala	Ala	Val	Ala	Ala	Ala	Leu
1				5				10						15
Leu	Leu	Val	Leu	Leu	Gly	Ala	Arg	Ala	Gln	Gly	Gly	Thr	Arg	Ser
			20						25					30
Pro	Arg	Cys	Asp	Cys	Ala	Gly	Asp	Phe	His	Lys	Lys	Ile	Gly	Leu
				35					40					45
Phe	Cys	Cys	Arg	Gly	Cys	Pro	Ala	Gly	His	Tyr	Leu	Lys	Ala	Pro
				50					55					60
Cys	Thr	Glu	Pro	Cys	Gly	Asn	Ser	Thr	Cys	Leu	Val	Cys	Pro	Gln
				65					70					75
Asp	Thr	Phe	Leu	Ala	Trp	Glu	Asn	His	His	Asn	Ser	Glu	Cys	Ala
				80					85					90
Arg	Cys	Gln	Ala	Cys	Asp	Glu	Gln	Ala	Ser	Gln	Val	Ala	Leu	Glu
				95					100					105
Asn	Cys	Ser	Ala	Val	Ala	Asp	Thr	Arg	Cys	Gly	Cys	Lys	Pro	Gly
				110					115					120
Trp	Phe	Val	Glu	Cys	Gln	Val	Ser	Gln	Cys	Val	Ser	Ser	Ser	Pro
				125					130					135
Phe	Tyr	Cys	Gln	Pro	Cys	Leu	Asp	Cys	Gly	Ala	Leu	His	Arg	His
				140					145					150
Thr	Arg	Leu	Leu	Cys	Ser	Arg	Arg	Asp	Thr	Asp	Cys	Gly	Thr	Cys
				155					160					165
Leu	Pro	Gly	Phe	Tyr	Glu	His	Gly	Asp	Gly	Cys	Val	Ser	Cys	Pro
				170					175					180

Thr

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 433 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTGCTGGGGG CCCGGGCCAG NGGCGGCACT CGTAGCCCCA GGTGTGACTG 50  
 TGCCGGTGAC TTCCACAAGA AGATTGGTCT GTTTTGTGTC AGAGGCTGCC 100  
 CAGCGGGGCA ACTACCTGAA GGCCCTTGC ACGGAGCCCT GCGCAACTCC 150  
 ACCTGCCTTG TGTGTCCCCA AGACACCTTC TTGGCCTGGG AGAACCACCA 200  
 TAATTCTGAA TGTGCCCCGCT GCCAGGCCTG TGATGAGCAG GCCTCCCAGG 250  
 TGGCGCTGGA GAACTGTTCA GCAGTGGCCG ACACCCGCTG TGGCTGTAAG 300  
 CAGGGCTGGT TTGTGGAGTG CCAGGGTCAG CCAATGTGTC AGCAGTTTCA 350

CCCTTCTAAT GCCAACCATG CCTAGACTGC GGGGCCCTGC AACGCAACAC 400

ACGGCTAATN TGTTTCCCGC AGAGATNATT GTT 433

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCGCTGCCA GGCCTGTGAT GAGCAGGC 28

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAGGGCCCCG CAGTCTAGGC ATGGTTGG 28

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1438 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCCGGC GCGGAGGCCG AGAGAGAAGT CACTTGCCCT GGCTCTACCT 50  
TGAAGTGGTT CTCAGGGTTG GGGCGAGAGT CGGGGTGGGG ACCGAGATGC 100  
AGCTCTATCC TGTGCCCCTG GTCGCAGCAG GCAGCCCAGC GCTTCGCGTG 150  
TTCTACTTGG CCTGTCCGCT GCCGCCTAAT GAGCTCAGGT CTAGGCCGAG 200  
CAGAGGGGGC ACCTGGTCGG ACTCGGTTGG GCTCGGGCGG CCCC GCCTCC 250  
CCCCGCCCCG CAGGCGGGCC CTTCTCGACG GCGCGGGGCG GGCCCTGCGG 300  
GCGCGGGGCT GAAGGCGGAA CCACGACGGG CAGAGAGCAC GGAGCCGGGA 350  
AGCCCCTGGG CGCCCGTCGG AGGGCTATGG AGCAGCGGCC GCGGGGCTGC 400  
GCGGCGGTGG CGGCGGCGCT CCTCCTGGTG CTGCTGGGGG CCCGGGCCCA 450  
GGGCGGCACT CGTAGCCCCA GGTGTGACTG TGCCGGTGAC TTCCACAAGA 500  
AGATTGGTCT GTTTTGTTGC AGAGGCTGCC CAGCGGGGCA CTACCTGAAG 550

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GCCCCTTGCA CGGAGCCCTG CGGCAACTCC ACCTGCCTTG TGTGTCCCCA 600  
 AGACACCTTC TTGGCCTGGG AGAACCACCA TAATTCTGAA TGTGCCCGCT 650  
 GCCAGGCCTG TGATGAGCAG GCCTCCCAGG TGGCGCTGGA GAACTGTTCA 700  
 GCAGTGGCCG ACACCCGCTG TGGCTGTAAG CCAGGCTGGT TTGTGGAGTG 750  
 CCAGGTCAGC CAATGTGTCA GCAGTTCACC CTTCTACTGC CAACCATGCC 800  
 TAGACTGCGG GGCCCTGCAC CGCCACACAC GGCTACTCTG TTCCCGCAGA 850  
 GATACTGACT GTGGGACCTG CCTGCCTGGC TTCTATGAAC ATGGCGATGG 900  
 CTGCGTGTCC TGCCCCACGT AATTCCTAGC TGTCGTGGGA TGGAGGGAAG 950  
 GCGGGCTGGG AGCAGAGCAG GGGCCTGGGG TGGGGCAGGT GCTGCTGGTT 1000  
 CAGGAATAGG AAGAGGGGAT AGGGAGGAGG GAGCCTTGGC CCTGTGATGG 1050  
 GTGGGCCCCA CTTCAAGCAA ACTTAGATGG CAAAAGAGCA ATCTGGATCC 1100  
 GCCTTAGCCA GATACATAAG GGTATTTGCC TTCACTTTCA GCCAGCATTC 1150  
 CCCCCAGCGA TCCTAGCCAG ATATTACAGA TGATTTGTCA CTTACACAGA 1200  
 GAGTCACATT GATATAGCTT TAAAACTTGG GCTGAAGGAG GTTGAGGCTG 1250  
 CAGTGAGCTA TGATCGTGCC ACTGCACTTC AGCCTGGGCA ACAGAGCGAG 1300  
 ACCTATTAAA TAAATAAATA AATATTAAAT CTATTAAATA TTAAATATTA 1350  
 AATCTATTAA ATAAATAAAT ACAAAGGGCT GAGAGTCAGG ACTGTGCTGC 1400  
 TAGTTCTCTA GGGGATCTTG GGCAAGTGCA GAGAATTC 1438

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 417 amino acids
  - (B) TYPE: Amino Acid
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Glu	Gln	Arg	Pro	Arg	Gly	Cys	Ala	Ala	Val	Ala	Ala	Ala	Leu
1				5					10					15
Leu	Leu	Val	Leu	Leu	Gly	Ala	Arg	Ala	Gln	Gly	Gly	Thr	Arg	Ser
			20						25					30
Pro	Arg	Cys	Asp	Cys	Ala	Gly	Asp	Phe	His	Lys	Lys	Ile	Gly	Leu
			35						40					45
Phe	Cys	Cys	Arg	Gly	Cys	Pro	Ala	Gly	His	Tyr	Leu	Lys	Ala	Pro
			50						55					60
Cys	Thr	Glu	Pro	Cys	Gly	Asn	Ser	Thr	Cys	Leu	Val	Cys	Pro	Gln
			65						70					75
Asp	Thr	Phe	Leu	Ala	Trp	Glu	Asn	His	His	Asn	Ser	Glu	Cys	Ala
			80						85					90

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Arg	Cys	Gln	Ala	Cys 95	Asp	Glu	Gln	Ala	Ser 100	Gln	Val	Ala	Leu	Glu 105
Asn	Cys	Ser	Ala	Val 110	Ala	Asp	Thr	Arg	Cys 115	Gly	Cys	Lys	Pro	Gly 120
Trp	Phe	Val	Glu	Cys 125	Gln	Val	Ser	Gln	Cys 130	Val	Ser	Ser	Ser	Pro 135
Phe	Tyr	Cys	Gln	Pro 140	Cys	Leu	Asp	Cys	Gly 145	Ala	Leu	His	Arg	His 150
Thr	Arg	Leu	Leu	Cys 155	Ser	Arg	Arg	Asp	Thr 160	Asp	Cys	Gly	Thr	Cys 165
Leu	Pro	Gly	Phe	Tyr 170	Glu	His	Gly	Asp	Gly 175	Cys	Val	Ser	Cys	Pro 180
Thr	Ser	Thr	Leu	Gly 185	Ser	Cys	Pro	Glu	Arg 190	Cys	Ala	Ala	Val	Cys 195
Gly	Trp	Arg	Gln	Met 200	Phe	Trp	Val	Gln	Val 205	Leu	Leu	Ala	Gly	Leu 210
Val	Val	Pro	Leu	Leu 215	Leu	Gly	Ala	Thr	Leu 220	Thr	Tyr	Thr	Tyr	Arg 225
His	Cys	Trp	Pro	His 230	Lys	Pro	Leu	Val	Thr 235	Ala	Asp	Glu	Ala	Gly 240
Met	Glu	Ala	Leu	Thr 245	Pro	Pro	Pro	Ala	Thr 250	His	Leu	Ser	Pro	Leu 255
Asp	Ser	Ala	His	Thr 260	Leu	Leu	Ala	Pro	Pro 265	Asp	Ser	Ser	Glu	Lys 270
Ile	Cys	Thr	Val	Gln 275	Leu	Val	Gly	Asn	Ser 280	Trp	Thr	Pro	Gly	Tyr 285
Pro	Glu	Thr	Gln	Glu 290	Ala	Leu	Cys	Pro	Gln 295	Val	Thr	Trp	Ser	Trp 300
Asp	Gln	Leu	Pro	Ser 305	Arg	Ala	Leu	Gly	Pro 310	Ala	Ala	Ala	Pro	Thr 315
Leu	Ser	Pro	Glu	Ser 320	Pro	Ala	Gly	Ser	Pro 325	Ala	Met	Met	Leu	Gln 330
Pro	Gly	Pro	Gln	Leu 335	Tyr	Asp	Val	Met	Asp 340	Ala	Val	Pro	Ala	Arg 345
Arg	Trp	Lys	Glu	Phe 350	Val	Arg	Thr	Leu	Gly 355	Leu	Arg	Glu	Ala	Glu 360
Ile	Glu	Ala	Val	Glu 365	Val	Glu	Ile	Gly	Arg 370	Phe	Arg	Asp	Gln	Gln 375
Tyr	Glu	Met	Leu	Lys 380	Arg	Trp	Arg	Gln	Gln 385	Gln	Pro	Ala	Gly	Leu 390
Gly	Ala	Val	Tyr	Ala 395	Ala	Leu	Glu	Arg	Met 400	Gly	Leu	Asp	Gly	Cys 405

Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly Pro  
410 415

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGCGCTCTGG TGGCCCTTGC AGAAGCC 27

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTCGGCCGAG AAGTTGAGAA ATGTC 25

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1634 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGGGCCCTGC GGGCGCGGGG CTGAAGGCGG AACCACGACG GGCAGAGAGC 50

ACGGAGCCGG GAAGCCCCTG GGCGCCCGTC GGAGGGCT ATG GAG 94  
Met Glu  
1

CAG CGG CCG CGG GGC TGC GCG GCG GTG GCG GCG GCG CTC 133  
Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu  
5 10 15

CTC CTG GTG CTG CTG GGG GCC CGG GCC CAG GGC GGC ACT 172  
Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr  
20 25

CGT AGC CCC AGG TGT GAC TGT GCC GGT GAC TTC CAC AAG 211  
Arg Ser Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys  
30 35 40

AAG ATT GGT CTG TTT TGT TGC AGA GGC TGC CCA GCG GGG 250  
Lys Ile Gly Leu Phe Cys Cys Arg Gly Cys Pro Ala Gly  
45 50

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CAC	TAC	CTG	AAG	GCC	CCT	TGC	ACG	GAG	CCC	TGC	GGC	AAC	289
His	Tyr	Leu	Lys	Ala	Pro	Cys	Thr	Glu	Pro	Cys	Gly	Asn	
55					60					65			
TCC	ACC	TGC	CTT	GTG	TGT	CCC	CAA	GAC	ACC	TTC	TTG	GCC	328
Ser	Thr	Cys	Leu	Val	Cys	Pro	Gln	Asp	Thr	Phe	Leu	Ala	
		70					75					80	
TGG	GAG	AAC	CAC	CAT	AAT	TCT	GAA	TGT	GCC	CGC	TGC	CAG	367
Trp	Glu	Asn	His	His	Asn	Ser	Glu	Cys	Ala	Arg	Cys	Gln	
				85					90				
GCC	TGT	GAT	GAG	CAG	GCC	TCC	CAG	GTG	GCG	CTG	GAG	AAC	406
Ala	Cys	Asp	Glu	Gln	Ala	Ser	Gln	Val	Ala	Leu	Glu	Asn	
	95					100					105		
TGT	TCA	GCA	GTG	GCC	GAC	ACC	CGC	TGT	GGC	TGT	AAG	CCA	445
Cys	Ser	Ala	Val	Ala	Asp	Thr	Arg	Cys	Gly	Cys	Lys	Pro	
			110					115					
GGC	TGG	TTT	GTG	GAG	TGC	CAG	GTC	AGC	CAA	TGT	GTC	AGC	484
Gly	Trp	Phe	Val	Glu	Cys	Gln	Val	Ser	Gln	Cys	Val	Ser	
120					125					130			
AGT	TCA	CCC	TTC	TAC	TGC	CAA	CCA	TGC	CTA	GAC	TGC	GGG	523
Ser	Ser	Pro	Phe	Tyr	Cys	Gln	Pro	Cys	Leu	Asp	Cys	Gly	
		135					140					145	
GCC	CTG	CAC	CGC	CAC	ACA	CGG	CTA	CTC	TGT	TCC	CGC	AGA	562
Ala	Leu	His	Arg	His	Thr	Arg	Leu	Leu	Cys	Ser	Arg	Arg	
				150					155				
GAT	ACT	GAC	TGT	GGG	ACC	TGC	CTG	CCT	GGC	TTC	TAT	GAA	601
Asp	Thr	Asp	Cys	Gly	Thr	Cys	Leu	Pro	Gly	Phe	Tyr	Glu	
	160					165					170		
CAT	GGC	GAT	GGC	TGC	GTG	TCC	TGC	CCC	ACG	AGC	ACC	CTG	640
His	Gly	Asp	Gly	Cys	Val	Ser	Cys	Pro	Thr	Ser	Thr	Leu	
			175					180					
GGG	AGC	TGT	CCA	GAG	CGC	TGT	GCC	GCT	GTC	TGT	GGC	TGG	679
Gly	Ser	Cys	Pro	Glu	Arg	Cys	Ala	Ala	Val	Cys	Gly	Trp	
185					190					195			
AGG	CAG	ATG	TTC	TGG	GTC	CAG	GTG	CTC	CTG	GCT	GGC	CTT	718
Arg	Gln	Met	Phe	Trp	Val	Gln	Val	Leu	Leu	Ala	Gly	Leu	
		200					205					210	
GTG	GTC	CCC	CTC	CTG	CTT	GGG	GCC	ACC	CTG	ACC	TAC	ACA	757
Val	Val	Pro	Leu	Leu	Leu	Gly	Ala	Thr	Leu	Thr	Tyr	Thr	
				215					220				
TAC	CGC	CAC	TGC	TGG	CCT	CAC	AAG	CCC	CTG	GTT	ACT	GCA	796
Tyr	Arg	His	Cys	Trp	Pro	His	Lys	Pro	Leu	Val	Thr	Ala	
	225					230					235		
GAT	GAA	GCT	GGG	ATG	GAG	GCT	CTG	ACC	CCA	CCA	CCG	GCC	835
Asp	Glu	Ala	Gly	Met	Glu	Ala	Leu	Thr	Pro	Pro	Pro	Ala	
			240					245					
ACC	CAT	CTG	TCA	CCC	TTG	GAC	AGC	GCC	CAC	ACC	CTT	CTA	874
Thr	His	Leu	Ser	Pro	Leu	Asp	Ser	Ala	His	Thr	Leu	Leu	
250					255					260			

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GCA	CCT	CCT	GAC	AGC	AGT	GAG	AAG	ATC	TGC	ACC	GTC	CAG	913
Ala	Pro	Pro	Asp	Ser	Ser	Glu	Lys	Ile	Cys	Thr	Val	Gln	275
		265					270						
TTG	GTG	GGT	AAC	AGC	TGG	ACC	CCT	GGC	TAC	CCC	GAG	ACC	952
Leu	Val	Gly	Asn	Ser	Trp	Thr	Pro	Gly	Tyr	Pro	Glu	Thr	
				280					285				
CAG	GAG	GCG	CTC	TGC	CCG	CAG	GTG	ACA	TGG	TCC	TGG	GAC	991
Gln	Glu	Ala	Leu	Cys	Pro	Gln	Val	Thr	Trp	Ser	Trp	Asp	
	290					295					300		
CAG	TTG	CCC	AGC	AGA	GCT	CTT	GGC	CCC	GCT	GCT	GCG	CCC	1030
Gln	Leu	Pro	Ser	Arg	Ala	Leu	Gly	Pro	Ala	Ala	Ala	Pro	
			305					310					
ACA	CTC	TCG	CCA	GAG	TCC	CCA	GCC	GGC	TCG	CCA	GCC	ATG	1069
Thr	Leu	Ser	Pro	Glu	Ser	Pro	Ala	Gly	Ser	Pro	Ala	Met	
					320					325			
ATG	CTG	CAG	CCG	GGC	CCG	CAG	CTC	TAC	GAC	GTG	ATG	GAC	1108
Met	Leu	Gln	Pro	Gly	Pro	Gln	Leu	Tyr	Asp	Val	Met	Asp	
		330					335					340	
GCG	GTC	CCA	GCG	CGG	CGC	TGG	AAG	GAG	TTC	GTG	CGC	ACG	1147
Ala	Val	Pro	Ala	Arg	Arg	Trp	Lys	Glu	Phe	Val	Arg	Thr	
				345					350				
CTG	GGG	CTG	CGC	GAG	GCA	GAG	ATC	GAA	GCC	GTG	GAG	GTG	1186
Leu	Gly	Leu	Arg	Glu	Ala	Glu	Ile	Glu	Ala	Val	Glu	Val	
	355					360					365		
GAG	ATC	GGC	CGC	TTC	CGA	GAC	CAG	CAG	TAC	GAG	ATG	CTC	1225
Glu	Ile	Gly	Arg	Phe	Arg	Asp	Gln	Gln	Tyr	Glu	Met	Leu	
			370					375					
AAG	CGC	TGG	CGC	CAG	CAG	CAG	CCC	GCG	GGC	CTC	GGA	GCC	1264
Lys	Arg	Trp	Arg	Gln	Gln	Gln	Pro	Ala	Gly	Leu	Gly	Ala	
					385					390			
GTT	TAC	GCG	GCC	CTG	GAG	CGC	ATG	GGG	CTG	GAC	GGC	TGC	1303
Val	Tyr	Ala	Ala	Leu	Glu	Arg	Met	Gly	Leu	Asp	Gly	Cys	
		395					400					405	
GTG	GAA	GAC	TTG	CGC	AGC	CGC	CTG	CAG	CGC	GGC	CCG	T	1340
Val	Glu	Asp	Leu	Arg	Ser	Arg	Leu	Gln	Arg	Gly	Pro		
				410					415		417		
GACACGGCGC	CCACTTGCCA	CCTAGGCGCT	CTGGTGGCCC	TTGCAGAAGC									1390
CCTAAGTACG	GTTACTTATG	CGTGTAGACA	TTTTATGTCA	CTTATTAAGC									1440
CGCTGGCACG	GCCCTGCGTA	GCAGCACCAG	CCGGCCCCAC	CCCTGCTCGC									1490
CCCTATCGCT	CCAGCCAAGG	CGAAGAAGCA	CGAACGAATG	TCGAGAGGGG									1540
GTGAAGACAT	TTCTCAACTT	CTCGGCCGGA	GTTTGGCTGA	GATCGCGGTA									1590
TTAAATCTGT	GAAAGAAAAC	AAAAAAAAAA	AAAAAAAAAA	AAAA									1634

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATCAGGGACT TTCCGCTGGG GACTTTCCG 29

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGGATGGGAA GTGTGTGATA TATCCTTGAT 30

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Val	Cys	Pro	Gln	Gly	Lys	Tyr	Ile	His	Pro	Gln	Asn	Asn	Ser	Ile	1	5	10	15
Cys	Cys	Thr	Lys	Cys	His	Lys	Gly	Thr	Tyr	Leu	Tyr	Asn	Asp	Cys	20	25	30	
Pro	Gly	Pro	Gly	Gln	Asp	Thr	Asp	Cys	Arg	Glu	Cys	Glu	Ser	Gly	35	40	45	
Ser	Phe	Thr	Ala	Ser	Glu	Asn	His	Leu	Arg	His	Cys	Leu	Ser	Cys	50	55	60	
Ser	Lys	Cys	Arg	Lys	Glu	Met	Gly	Gln	Val	Glu	Ile	Ser	Ser	Cys	65	70	75	
Thr	Val	Asp	Arg	Asp	Thr	Val	Cys	Gly	Cys	Arg	Lys	Asn	Gln	Tyr	80	85	90	
Arg	His	Tyr	Trp	Ser	Glu	Asn	Leu	Phe	Gln	Cys	Phe	Asn	Cys	Ser	95	100	105	
Leu	Cys	Leu	Asn	Gly	Thr	Val	His	Leu	Ser	Cys	Gln	Glu	Lys	Gln	110	115	120	
Asn	Thr	Val	Cys	Thr	Cys	His	Ala	Gly	Phe	Phe	Leu	Arg	Glu	Asn	125	130	135	
Glu	Cys	Val	Ser	Cys	Ser	Asn	Cys	Lys	Lys	Ser	Leu	Glu	Cys	Thr	140	145	150	

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Lys Leu Cys Leu

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 163 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Thr	Cys	Arg	Leu	Arg	Glu	Tyr	Tyr	Asp	Gln	Thr	Ala	Gln	Met	Cys
1				5					10					15
Cys	Ser	Lys	Cys	Ser	Pro	Gly	Gln	His	Ala	Lys	Val	Phe	Cys	Thr
				20					25					30
Lys	Thr	Ser	Asp	Thr	Val	Cys	Asp	Ser	Cys	Glu	Asp	Ser	Thr	Tyr
				35					40					45
Thr	Gln	Leu	Trp	Asn	Trp	Val	Pro	Glu	Cys	Leu	Ser	Cys	Gly	Ser
				50					55					60
Arg	Cys	Ser	Ser	Asp	Gln	Val	Glu	Thr	Gln	Ala	Cys	Thr	Arg	Glu
				65					70					75
Gln	Asn	Arg	Ile	Cys	Thr	Cys	Arg	Pro	Gly	Trp	Tyr	Cys	Ala	Leu
				80					85					90
Ser	Lys	Gln	Glu	Gly	Cys	Arg	Leu	Cys	Ala	Pro	Leu	Arg	Lys	Cys
				95					100					105
Arg	Pro	Gly	Phe	Gly	Val	Ala	Arg	Pro	Gly	Thr	Glu	Thr	Ser	Asp
				110					115					120
Val	Val	Cys	Lys	Pro	Cys	Ala	Pro	Gly	Thr	Phe	Ser	Asn	Thr	Thr
				125					130					135
Ser	Ser	Thr	Asp	Ile	Cys	Arg	Pro	His	Gln	Ile	Cys	Asn	Val	Val
				140					145					150
Ala	Ile	Pro	Gly	Asn	Ala	Ser	Arg	Asp	Ala	Val	Cys	Thr		
				155					160					

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 170 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Thr	Cys	Arg	Asp	Gln	Glu	Lys	Glu	Tyr	Tyr	Glu	Pro	Gln	His	Arg
1				5					10					15
Ile	Cys	Cys	Ser	Arg	Cys	Pro	Pro	Gly	Thr	Tyr	Val	Ser	Ala	Lys
				20					25					30
Cys	Ser	Arg	Ile	Arg	Asp	Thr	Val	Cys	Ala	Thr	Cys	Ala	Glu	Asn
				35					40					45

P1007P1D1seq1 (new)-response to 6-29-04 action.txt

Ser	Tyr	Asn	Glu	His	Trp	Asn	Tyr	Leu	Thr	Ile	Cys	Gln	Leu	Cys
				50					55					60
Arg	Pro	Cys	Asp	Pro	Val	Met	Gly	Leu	Glu	Glu	Ile	Ala	Pro	Cys
				65					70					75
Thr	Ser	Lys	Arg	Lys	Thr	Gln	Cys	Arg	Cys	Gln	Pro	Gly	Met	Phe
				80					85					90
Cys	Ala	Ala	Trp	Ala	Leu	Glu	Cys	Thr	His	Cys	Glu	Leu	Leu	Ser
				95					100					105
Asp	Cys	Pro	Pro	Gly	Thr	Glu	Ala	Glu	Leu	Lys	Asp	Glu	Val	Gly
				110					115					120
Lys	Gly	Asn	Asn	His	Cys	Val	Pro	Cys	Lys	Ala	Gly	His	Phe	Gln
				125					130					135
Asn	Thr	Ser	Ser	Pro	Ser	Ala	Arg	Cys	Gln	Pro	His	Thr	Arg	Cys
				140					145					150
Glu	Asn	Gln	Gly	Leu	Val	Glu	Ala	Ala	Pro	Gly	Thr	Ala	Gln	Ser
				155					160					165
Asp	Thr	Thr	Cys	Lys										
				170										

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 119 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Asn	Leu	Glu	Gly	Leu	His	His	Asp	Gly	Gln	Phe	Cys	His	Lys	Pro
1				5					10					15
Cys	Pro	Pro	Gly	Glu	Arg	Lys	Ala	Arg	Asp	Cys	Thr	Val	Asn	Gly
				20					25					30
Asp	Glu	Pro	Asp	Cys	Val	Pro	Cys	Gln	Glu	Gly	Lys	Glu	Tyr	Thr
				35					40					45
Asp	Lys	Ala	His	Phe	Ser	Ser	Lys	Cys	Arg	Arg	Cys	Arg	Leu	Cys
				50					55					60
Asp	Glu	Gly	His	Gly	Leu	Glu	Val	Glu	Ile	Asn	Cys	Thr	Arg	Thr
				65					70					75
Gln	Asn	Thr	Lys	Cys	Arg	Cys	Lys	Pro	Asn	Phe	Phe	Cys	Asn	Ser
				80					85					90
Thr	Val	Cys	Glu	His	Cys	Asp	Pro	Cys	Thr	Lys	Cys	Glu	His	Gly
				95					100					105
Ile	Ile	Lys	Glu	Cys	Thr	Leu	Thr	Ser	Asn	Thr	Lys	Cys	Lys	
				110					115					

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:

P1007P1D1seq1 (new)-response to 6-29-04 action.txt

(A) LENGTH: 159 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ala	Cys	Pro	Thr	Gly	Leu	Tyr	Thr	His	Ser	Gly	Glu	Cys	Cys	Lys
1				5					10					15
Ala	Cys	Asn	Leu	Gly	Glu	Gly	Val	Ala	Gln	Pro	Cys	Gly	Ala	Asn
				20					25					30
Gln	Thr	Val	Cys	Glu	Pro	Cys	Leu	Asp	Ser	Val	Thr	Phe	Ser	Asp
				35					40					45
Val	Val	Ser	Ala	Thr	Glu	Pro	Cys	Lys	Pro	Cys	Thr	Glu	Cys	Val
				50					55					60
Gly	Leu	Gln	Ser	Met	Ser	Ala	Pro	Cys	Val	Glu	Ala	Asp	Asp	Ala
				65					70					75
Val	Cys	Arg	Cys	Ala	Tyr	Gly	Tyr	Tyr	Gln	Asp	Glu	Thr	Thr	Gly
				80					85					90
Arg	Cys	Glu	Ala	Cys	Arg	Val	Cys	Glu	Ala	Gly	Ser	Gly	Leu	Val
				95					100					105
Phe	Ser	Cys	Gln	Asp	Lys	Gln	Asn	Thr	Val	Cys	Glu	Glu	Cys	Pro
				110					115					120
Asp	Gly	Thr	Tyr	Ser	Asp	Glu	Ala	Asn	His	Val	Asp	Pro	Cys	Leu
				125					130					135
Pro	Cys	Thr	Val	Cys	Glu	Asp	Thr	Glu	Arg	Gln	Leu	Arg	Glu	Cys
				140					145					150
Thr	Arg	Trp	Ala	Asp	Ala	Glu	Cys	Glu						
				155										

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 163 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Ala	Cys	Arg	Glu	Lys	Gln	Tyr	Leu	Ile	Asn	Ser	Gln	Cys	Cys	Ser
1				5					10					15
Leu	Cys	Gln	Pro	Gly	Gln	Lys	Leu	Val	Ser	Asp	Cys	Thr	Glu	Phe
				20					25					30
Thr	Glu	Thr	Glu	Cys	Leu	Pro	Cys	Gly	Glu	Ser	Glu	Phe	Leu	Asp
				35					40					45
Thr	Trp	Asn	Arg	Glu	Thr	His	Cys	His	Gln	His	Lys	Tyr	Cys	Asp
				50					55					60
Pro	Asn	Leu	Gly	Leu	Arg	Val	Gln	Gln	Lys	Gly	Thr	Ser	Glu	Thr
				65					70					75

P1007P1D1seq1 (new)-response to 6-29-04 action.txt

Asp	Thr	Ile	Cys	Thr	Cys	Glu	Glu	Gly	Trp	His	Cys	Thr	Ser	Glu
				80					85					90
Ala	Cys	Glu	Ser	Cys	Val	Leu	His	Arg	Ser	Cys	Ser	Pro	Gly	Phe
				95					100					105
Gly	Val	Lys	Gln	Ile	Ala	Thr	Gly	Val	Ser	Asp	Thr	Ile	Cys	Glu
				110					115					120
Pro	Cys	Pro	Val	Gly	Phe	Phe	Ser	Asn	Val	Ser	Ser	Ala	Phe	Glu
				125					130					135
Lys	Cys	His	Pro	Trp	Thr	Ser	Cys	Glu	Thr	Lys	Asp	Leu	Val	Val
				140					145					150
Gln	Gln	Ala	Gly	Thr	Asn	Lys	Thr	Asp	Val	Val	Cys	Gly		
				155					160					

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 121 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ser	Cys	Pro	Glu	Arg	His	Tyr	Trp	Ala	Gln	Gly	Lys	Leu	Cys	Cys
1				5					10					15
Gln	Met	Cys	Glu	Pro	Gly	Thr	Phe	Leu	Val	Lys	Asp	Cys	Asp	Gln
				20					25					30
His	Arg	Lys	Ala	Ala	Gln	Cys	Asp	Pro	Cys	Ile	Pro	Gly	Val	Ser
				35					40					45
Phe	Ser	Pro	Asp	His	His	Thr	Arg	Pro	His	Cys	Glu	Ser	Cys	Arg
				50					55					60
His	Cys	Asn	Ser	Gly	Leu	Leu	Val	Arg	Asn	Cys	Thr	Ile	Thr	Ala
				65					70					75
Asn	Ala	Glu	Cys	Ala	Cys	Arg	Asn	Gly	Trp	Gln	Cys	Arg	Asp	Lys
				80					85					90
Glu	Cys	Thr	Glu	Cys	Asp	Pro	Leu	Pro	Asn	Pro	Ser	Leu	Thr	Ala
				95					100					105
Arg	Ser	Ser	Gln	Ala	Leu	Ser	Pro	His	Pro	Gln	Pro	Thr	His	Leu
				110					115					120

Pro

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 123 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

P1007P1D1seq1 (new)-response to 6-29-04 action.txt

Thr	Cys	His	Gly	Asn	Pro	Ser	His	Tyr	Tyr	Asp	Lys	Ala	Val	Arg
1				5					10					15
Arg	Cys	Cys	Tyr	Arg	Cys	Pro	Met	Gly	Leu	Phe	Pro	Thr	Gln	Gln
				20					25					30
Cys	Pro	Gln	Arg	Pro	Thr	Asp	Cys	Arg	Lys	Gln	Cys	Glu	Pro	Asp
				35					40					45
Tyr	Tyr	Leu	Asp	Glu	Ala	Asp	Arg	Cys	Thr	Ala	Cys	Val	Thr	Cys
				50					55					60
Ser	Arg	Asp	Asp	Leu	Val	Glu	Lys	Thr	Pro	Cys	Ala	Trp	Asn	Ser
				65					70					75
Ser	Arg	Val	Cys	Glu	Cys	Arg	Pro	Gly	Met	Phe	Cys	Ser	Thr	Ser
				80					85					90
Ala	Val	Asn	Ser	Cys	Ala	Arg	Cys	Phe	Phe	His	Ser	Val	Cys	Pro
				95					100					105
Ala	Gly	Met	Ile	Val	Lys	Phe	Pro	Gly	Thr	Ala	Gln	Lys	Asn	Thr
				110					115					120
Val	Cys	Glu												

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 138 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

His	Cys	Val	Gly	Asp	Thr	Tyr	Pro	Ser	Asn	Asp	Arg	Cys	Cys	His
1				5					10					15
Glu	Cys	Arg	Pro	Gly	Asn	Gly	Met	Val	Ser	Arg	Cys	Ser	Arg	Ser
				20					25					30
Gln	Asn	Thr	Val	Cys	Arg	Pro	Cys	Gly	Pro	Gly	Phe	Tyr	Asn	Asp
				35					40					45
Val	Val	Ser	Ser	Lys	Pro	Cys	Lys	Pro	Cys	Thr	Trp	Cys	Asn	Leu
				50					55					60
Arg	Ser	Gly	Ser	Glu	Arg	Lys	Gln	Leu	Cys	Thr	Ala	Thr	Gln	Asp
				65					70					75
Thr	Val	Cys	Arg	Cys	Arg	Ala	Gly	Thr	Gln	Pro	Leu	Asp	Ser	Tyr
				80					85					90
Lys	Pro	Gly	Val	Asp	Cys	Ala	Pro	Cys	Pro	Pro	Gly	His	Phe	Ser
				95					100					105
Pro	Gly	Asp	Asn	Gln	Ala	Cys	Lys	Pro	Trp	Thr	Asn	Cys	Thr	Leu
				110					115					120
Ala	Gly	Lys	His	Thr	Leu	Gln	Pro	Ala	Ser	Asn	Ser	Ser	Asp	Ala
				125					130					135

Ile Cys Glu

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 197 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met	Gly	Leu	Ser	Thr	Val	Pro	Asp	Leu	Leu	Leu	Pro	Leu	Val	Leu	1	5	10	15
Leu	Glu	Leu	Leu	Val	Gly	Ile	Tyr	Pro	Ser	Gly	Val	Ile	Gly	Leu	20	25	30	
Val	Pro	His	Leu	Gly	Asp	Arg	Glu	Lys	Arg	Asp	Ser	Val	Cys	Pro	35	40	45	
Gln	Gly	Lys	Tyr	Ile	His	Pro	Gln	Asn	Asn	Ser	Ile	Cys	Cys	Thr	50	55	60	
Lys	Cys	His	Lys	Gly	Thr	Tyr	Leu	Tyr	Asn	Asp	Cys	Pro	Gly	Pro	65	70	75	
Gly	Gln	Asp	Thr	Asp	Cys	Arg	Glu	Cys	Glu	Ser	Gly	Ser	Phe	Thr	80	85	90	
Ala	Ser	Glu	Asn	His	Leu	Arg	His	Cys	Leu	Ser	Cys	Ser	Lys	Cys	95	100	105	
Arg	Lys	Glu	Met	Gly	Gln	Val	Glu	Ile	Ser	Ser	Cys	Thr	Val	Asp	110	115	120	
Arg	Asp	Thr	Val	Cys	Gly	Cys	Arg	Lys	Asn	Gln	Tyr	Arg	His	Tyr	125	130	135	
Trp	Ser	Glu	Asn	Leu	Phe	Gln	Cys	Phe	Asn	Cys	Ser	Leu	Cys	Leu	140	145	150	
Asn	Gly	Thr	Val	His	Leu	Ser	Cys	Gln	Glu	Lys	Gln	Asn	Thr	Val	155	160	165	
Cys	Thr	Cys	His	Ala	Gly	Phe	Phe	Leu	Arg	Glu	Asn	Glu	Cys	Val	170	175	180	
Ser	Cys	Ser	Asn	Cys	Lys	Lys	Ser	Leu	Glu	Cys	Thr	Lys	Leu	Cys	185	190	195	

Leu Pro

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 167 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

P1007P1D1seq1 (new)-response to 6-29-04 action.txt

Met	Leu	Gly	Ile	Trp	Thr	Leu	Leu	Pro	Leu	Val	Leu	Thr	Ser	Val
1				5					10					15
Ala	Arg	Leu	Ser	Ser	Lys	Ser	Val	Asn	Ala	Gln	Val	Thr	Asp	Ile
				20					25					30
Asn	Ser	Lys	Gly	Leu	Glu	Leu	Arg	Lys	Thr	Val	Thr	Thr	Val	Glu
				35					40					45
Thr	Gln	Asn	Leu	Glu	Gly	Leu	His	His	Asp	Gly	Gln	Phe	Cys	His
				50					55					60
Lys	Pro	Cys	Pro	Pro	Gly	Glu	Arg	Lys	Ala	Arg	Asp	Cys	Thr	Val
				65					70					75
Asn	Gly	Asp	Glu	Pro	Asp	Cys	Val	Pro	Cys	Gln	Glu	Gly	Lys	Glu
				80					85					90
Tyr	Thr	Asp	Lys	Ala	His	Phe	Ser	Ser	Lys	Cys	Arg	Arg	Cys	Arg
				95					100					105
Leu	Cys	Asp	Glu	Gly	His	Gly	Leu	Glu	Val	Glu	Ile	Asn	Cys	Thr
				110					115					120
Arg	Thr	Gln	Asn	Thr	Lys	Cys	Arg	Cys	Lys	Pro	Asn	Phe	Phe	Cys
				125					130					135
Asn	Ser	Thr	Val	Cys	Glu	His	Cys	Asp	Pro	Cys	Thr	Lys	Cys	Glu
				140					145					150
His	Gly	Ile	Ile	Lys	Glu	Cys	Thr	Leu	Thr	Ser	Asn	Thr	Lys	Cys
				155					160					165

Lys Glu

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 78 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Val	Val	Glu	Asn	Val	Pro	Pro	Leu	Arg	Trp	Lys	Glu	Phe	Val	Arg
1				5					10					15
Arg	Leu	Gly	Leu	Ser	Asp	His	Glu	Ile	Asp	Arg	Leu	Glu	Leu	Gln
				20					25					30
Asn	Gly	Arg	Cys	Leu	Arg	Glu	Ala	Gln	Tyr	Ser	Met	Leu	Ala	Thr
				35					40					45
Trp	Arg	Arg	Arg	Thr	Pro	Arg	Arg	Glu	Ala	Thr	Leu	Glu	Leu	Leu
				50					55					60
Gly	Arg	Val	Leu	Arg	Asp	Met	Asp	Leu	Leu	Gly	Cys	Leu	Glu	Asp
				65					70					75

Ile Glu Glu

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 77 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ile Ala Gly Val Met Thr Leu Ser Gln Val Lys Gly Phe Val Arg  
 1 5 10 15  
 Lys Asn Gly Val Asn Glu Ala Lys Ile Asp Glu Ile Lys Asn Asp  
 20 25 30  
 Asn Val Gln Asp Thr Ala Glu Gln Lys Val Gln Leu Leu Arg Asn  
 35 40 45  
 Trp His Gln Leu His Gly Lys Lys Glu Ala Tyr Asp Thr Leu Ile  
 50 55 60  
 Lys Asp Leu Lys Lys Ala Asn Leu Cys Thr Leu Ala Glu Lys Ile  
 65 70 75  
 Gln Thr

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 74 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ile Cys Asp Asn Val Gly Lys Asp Trp Arg Arg Leu Ala Arg Gln  
 1 5 10 15  
 Leu Lys Val Ser Asp Thr Lys Ile Asp Ser Ile Glu Asp Arg Tyr  
 20 25 30  
 Pro Arg Asn Leu Thr Glu Arg Val Arg Glu Ser Leu Arg Ile Trp  
 35 40 45  
 Lys Asn Thr Glu Lys Glu Asn Ala Thr Val Ala His Leu Val Gly  
 50 55 60  
 Ala Leu Arg Ser Cys Gln Met Asn Leu Val Ala Asp Leu Val  
 65 70

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 77 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Asn Arg Pro Leu Ser Leu Lys Asp Gln Gln Thr Phe Ala Arg Ser  
 1 5 10 15

P1007P1D1seq1 (new)-response to 6-29-04 action.txt

Val Gly Leu Lys Trp Arg Lys Val Gly Arg Ser Leu Gln Arg Gly  
20 25 30  
Cys Arg Ala Leu Arg Asp Pro Ala Leu Asp Ser Leu Ala Tyr Glu  
35 40 45  
Tyr Glu Arg Glu Gly Leu Tyr Glu Gln Ala Phe Gln Leu Leu Arg  
50 55 60  
Arg Phe Val Gln Ala Glu Gly Arg Arg Ala Thr Leu Gln Arg Leu  
65 70 75  
Val Glu

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 77 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Ile Arg Glu Asn Leu Gly Lys His Trp Lys Asn Cys Ala Arg Lys  
1 5 10 15  
Leu Gly Phe Thr Gln Ser Gln Ile Asp Glu Ile Asp His Asp Tyr  
20 25 30  
Glu Arg Asp Gly Leu Lys Glu Lys Val Tyr Gln Met Leu Gln Lys  
35 40 45  
Trp Val Met Arg Glu Gly Ile Lys Gly Ala Thr Val Gly Lys Leu  
50 55 60  
Ala Gln Ala Leu His Gln Cys Ser Arg Ile Asp Leu Leu Ser Ser  
65 70 75  
Leu Thr

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 63 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Ala Val Ala Phe Tyr Ile Pro Asp Gln Ala Thr Leu Leu Arg  
1 5 10 15  
Glu Ala Glu Gln Lys Glu Gln Gln Ile Leu Arg Leu Arg Glu Ser  
20 25 30  
Gln Trp Arg Phe Leu Ala Thr Val Val Leu Glu Thr Leu Lys Gln  
35 40 45  
Tyr Thr Ser Cys His Pro Lys Thr Gly Arg Lys Ser Gly Lys Tyr  
50 55 60

Arg Lys Pro

P1007P1D1seq1 (new)-response to 6-29-04 action.txt